

## REMARKS

### **Status of the Claims**

Claims 1-34 are pending. Claims 31-33 were withdrawn from further consideration as a result of a restriction requirement by the Examiner, under 37 C.F.R. §1.142(b), in Paper No. 13.

In the instant Response, claims 21 and 31-33 are cancelled, without prejudice; claims 1-4, 6, 22-28, 30 and 34 are amended; and claims 35 and 36 are added. Thus, after entry of these amendments, claims 1-20, 22-30 and 34-36 are presented for consideration.

Pursuant to the Office Action, claims 1-30 and 34 are rejected under 35 U.S.C. §112, second paragraph. Claims 34, 1-12, and 18-20 are rejected under 35 U.S.C. §102 as alleged anticipated by Pellegrini *et al.* (1999) PNAS USA 96:4285-4288 (hereinafter "Pellegrini"). Claims 34, 2, 4, 5, 7, 8, and 21-30 are rejected under 35 U.S.C. §102 as allegedly anticipated by Marcotte *et al.* (1999) Science 285:751-753 (hereinafter "Marcotte"). Applicants respectfully traverse all outstanding objections to the specification and rejection of the claims.

### **Support for Claim Amendments**

Support for the claim amendments can be found throughout the specification. In particular, claim 34 has been amended and new claim 35 added to more particularly describe the invention. Support for biological and chemical properties of interest, and specific properties, can be found, *inter alia*, at page 2, lines 2-3 (where it is explained that two proteins can be considered functionally related if they form part of the same biochemical pathway or biological process); at lines 3-6 (which reference catalytic properties); at page 7, lines 7-17, and Figures 1-5 (which reference binding properties and cell membrane proteins whose property of cellular localization would be of interest). Accordingly, one skilled in the art would understand and recognize properties of interest in identifying proteins that are functionally related and useful for drug discovery and cell viability and growth.

New claim 36 describes with more particularity the domain fusion method of claim 21. Support for the claim can be found, *inter alia*, at page 10, lines 8-30. For example, proteins A and B may correspond to the first and second proteins of claim 36 step (a) and protein AB may correspond to the third protein of claim 36 step (b). Amendments to claims 1-4, 6, 22-28, and 30 merely reflect the cancellation of claim 21, amendments to claim 34 and addition of claim 36, as well as correct errors. Applicants submit that no new matter is introduced by the present amendment.

### **Informalities**

The specification is objected to because on page 7, line 14, there is a statement that begins "Figure shows," and it should be "Figure 4 shows." Applicants have amended the specification to overcome this objection.

### **Issues under 35 U.S.C. §112, second paragraph**

Claims 1-30 and 34 are rejected under 35 U.S.C. § 112, second paragraph, for allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as the invention.

The Patent Office alleges that claim 34 is indefinite because of the limitation "...nucleic acid or polypeptide sequence that may possess a property of interest functionally related to a first nucleic acid."<sup>1</sup> Applicants have amended claim 34 to more particularly describe the claimed invention.

The Patent Office alleges that claim 3 recites the limitation "the drug" in line 1 without sufficient antecedent basis.<sup>2</sup> Applicants have amended claim 3 to overcome this rejection.

The Patent Office alleges that claim 6 recites the limitation "the microorganism" in line 1 without sufficient antecedent basis.<sup>3</sup> Applicants have amended claim 6 to provide antecedent support.

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<sup>1</sup> See page 4, lines 4-7, of the Office Action.

<sup>2</sup> See page 4, lines 8-9, of the Office Action.

The Patent Office alleges that claim 30 is indefinite because the limitation "excessive functional links" is unclear.<sup>4</sup> Applicants respectfully submit that based upon the specification, the meaning of "excessive functional links" would be apparent to the skilled artisan. For example, on page 14, lines 19-24, of the specification, excessive functional links are those where the domain is linked to more than 25 other domains.

In light of the foregoing remarks and amendments, Applicants respectfully submit that the claims 1-20, 21-30, and 34 are in condition for allowance and respectfully request reconsideration and withdrawal of the rejection under 35 U.S.C. §112, second paragraph.

### **Issues under 35 U.S.C. §102**

Claims 34, 1-12, and 18-20 are rejected under 35 U.S.C. §102 for allegedly being anticipated by Pellegrini. Claims 34, 2, 4, 5, 7, 8, and 21-30 are rejected under 35 U.S.C. § 102 for allegedly being anticipated by Marcotte.

Applicants respectfully submit an unequivocal declaration under 37 CFR §1.132 that the subject matter disclosed in Pellegrini and Marcotte is their own work. Accordingly, the two references are not proper prior art as to the claimed invention. (See MPEP 716.10, *In re Katz*, 687 F.2d 450 (CCPA 1982).

In light of the foregoing reason, Applicants respectfully request reconsideration and withdrawal of the rejection under 35 U.S.C. §102 as allegedly anticipated by Pellegrini or Marcotte.

### **CONCLUSION**

Applicants request that the Examiner reconsider the application and claims in light of the foregoing reasons and amendments and respectfully submit that the claims are in condition for allowance.

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<sup>3</sup> See page 4, lines 10-11, of the Office Action.

<sup>4</sup> See page 4, lines 12-13, of the Office Action.

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If, in the Examiner's opinion, a telephonic interview would expedite the favorable prosecution of the present application, the undersigned attorney would welcome the opportunity to discuss any outstanding issues and to work with the Examiner toward placing the application in condition for allowance.

Attached is a marked-up version of the changes being made by the current amendment.

Applicants believe that no additional fees are necessitated by the present Response. However, in the event any such fees are due, the Commissioner is hereby authorized to charge any such fees to Deposit Account No. 06-1050.

Respectfully submitted,

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**Version with markings to show changes made**

In the specification:

Paragraph beginning on page 7, line 14, has been amended as follows:

Figure 4 shows that gcpE (Rv 2868C) is predicted to be functionally linked to cell wall metabolism.

In the claims:

Claim 21 is cancelled without prejudice.

Claims 1-4, 6, 21-28, 30, and 34 have been amended as follows:

1. (Twice amended) The method of claim 34, wherein the property of interest [of the first sequence] is a target for a drug.

2. (Twice amended) The method of claim 34, wherein the property of interest [of the first sequence] is a [sequence] protein essential for the growth or viability of an organism.

3. (Amended) The method of claim 1 [or claim 2], wherein the drug is an anti-microbial drug.

4. (Amended) The method of claim 1 or claim 2, wherein the first nucleic acid sequence or [a] polypeptide sequence is derived from a pathogen.

6. (Amended) The method of claim 4 [1 or claim 2], wherein the microorganism is *Mycobacterium tuberculosis* (MTB).

22. (Amended) The method of claim 36 [21], wherein the aligning is performed by an algorithm selected from the group consisting of a Smith-Waterman algorithm, Needleman-Wunsch algorithm, a BLAST algorithm, a FASTA algorithm, and a PSI-BLAST algorithm.

23. (Amended) The method of claim 36 [21], wherein at least one polypeptide sequence is [the multiple distinct non-homologous polypeptides are] obtained by translating a nucleic acid sequence from a genome database.

24. (Amended) The method of claim 36 [21], wherein the sequences are from a database [plurality of proteins have a known function].

25. (Amended) The method of claim 36 [21], wherein at least the first protein [one of the multiple distinct non-homologous polypeptides] has a known function.

26. (Amended) The method of claim 36 [21], wherein at least one of the proteins [multiple distinct non-homologous polypeptides] has an unknown function.

27. (Amended) The method of claim 36 [21], wherein the alignment is based on the degree of homology of the nucleic acid or polypeptide sequences of the first and second proteins to a segment of the nucleic acid or polypeptide sequence of the third protein [multiple distinct non-homologous polypeptides to the plurality of proteins].

28. (Amended) The method of claim 36 [21], further comprising determining the significance of the aligned and identified second nucleic acid or polypeptide [primary amino acid sequence] by computing a probability (p) value threshold.

30. (Amended) The method of claim 36 [21], further comprising filtering excessive functional links between the first protein and any second protein [one first primary amino acid sequence of multiple distinct non-homologous polypeptides and an excessive number of other distinct non-homologous polypeptides for any alignment found between the first primary amino acid sequences of the distinct non-homologous polypeptides and at least one of the second primary amino acid sequences of the plurality of proteins].

34. (Amended) A method for identifying a second nucleic acid sequence or second polypeptide sequence of a second protein, wherein the second protein has a biological or chemical [that may possess a] property of interest [functionally related to a first nucleic acid or a first polypeptide sequence], comprising [the following steps]:

(a) providing a first nucleic acid sequence or a first polypeptide sequence comprising the biological or chemical property of interest;

(b) providing at least one algorithm capable of analyzing a functional relationship between the first protein and second protein [nucleic acid or the polypeptide sequences] selected from the group consisting of a "domain fusion" method, a "phylogenetic profile" method, and a "physiologic linkage" method; and

(c) comparing the first nucleic acid sequence or the first polypeptide sequence to a plurality of sequences using at least one of the algorithms as set forth in step (b) to identify the [a] second nucleic acid sequence or [a] second polypeptide sequence of the second protein which [that] has a functional relationship to the first protein [nucleic acid or polypeptide sequence], thereby identifying a nucleic acid sequence or polypeptide sequence of a protein that possesses [may possess] the property of interest.